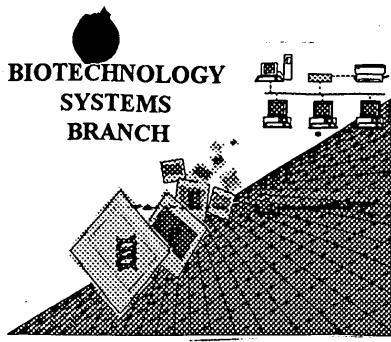# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical-Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/676,135_

Source: _OIPE_

Date Processed by STIC: _10/11/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

```
        RAW SEQUENCE LISTING              DATE: 10/11/2000
        PATENT APPLICATION:  US/09/676,135    TIME: 12:29:07

        Input Set : A:\ES.txt
        Output Set: N:\CRF3\10112000\I676135.raw
```

Does Not Comply
Corrected Diskette Needed

```
  3 <110> APPLICANT: Boyle, Brian J
  4        Mize, Nancy K
  5        Arterburn, Matthew C
  6        Yeung, George
  7        Tang, Y. Tom
  8        Liu, Chenghua
  9        Drmanac, Radoje T
 10        Wang, Menq-Yun
 11        Chen, Lichuan
 12        Yang, Yea-Huey
 14 <120> TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO METALLOCARBOXYPEPTIDASE-LIKE
 15        POLYPEPTIDES AND POLYNUCLEOTIDES
 17 <130> FILE REFERENCE: HYS-28
 19 <140> CURRENT APPLICATION NUMBER: US/09/676,135
 20 <141> CURRENT FILING DATE: 2000-09-29
 22 <150> PRIOR APPLICATION NUMBER: US 09/560,875
 23 <151> PRIOR FILING DATE: 2000-04-27
 25 <150> PRIOR APPLICATION NUMBER: US 09/496,914
 26 <151> PRIOR FILING DATE: 2000-02-03
 28 <160> NUMBER OF SEQ ID NOS: 22
 30 <170> SOFTWARE: PatentIn version 3.0
```

ERRORED SEQUENCES

```
      565 <210> SEQ ID NO: 19           /64 shown
      566 <211> LENGTH: 165
      567 <212> TYPE: PRT
      568 <213> ORGANISM: homo sapiens
      570 <400> SEQUENCE: 19
      572 Tyr Lys Glu Val Val Thr Gln His Phe Leu     Val Thr Tyr Glu Thr
E--> 573 1               5                   10                  15
      575 His Pro Ile Tyr Tyr Leu Lys Ile Ser Gln Pro Ser Gly Asn Pro Lys
E--> 576             20                  25                  30
      578 Lys Ile Ile Trp Met Asp Cys Gly Ile His Ala Arg Glu Trp Ile Ala
E--> 579             35                  40                  45
      581 Pro Ala Phe Cys Gln Trp Phe Val Lys Glu Ile Leu Gln Asn His Lys
E--> 582     50                  55                  60
      584 Asp Asn Ser Arg Ile Arg Lys Leu Leu Met Asn Leu Asp Phe Tyr Val
E--> 585 65                  70                  75                  80
      587 Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile Tyr Thr Trp Thr Thr Asp
E--> 588             85                  90                  95
      590 Arg Leu Trp Arg Lys Ser Arg Ser Pro His Asn Asn Gly Thr Cys Phe
E--> 591             100                 105                 110
      593 Gly Thr Asp Leu Asn Arg Asn Phe Asn Ala Ser Trp Cys Ser Ile Gly
E--> 594         115                 120                 125
      596 Ala Ser Arg Asn Cys Gln Asp Gln Thr Phe Cys Gly Thr Gly Pro Val
```

(handwritten annotation) why is a gap present? Per 1.822(e) of Sequence Rules, "A sequence with a gap or gaps shall be presented as a plurality of separate sequences, with separate sequence identifiers, with the number of separate sequences being equal in number to the number of continuous strings of sequence data." If gap represents a stop codon, amino acids following it need a separate sequence identifier.

```
                RAW SEQUENCE LISTING                 DATE: 10/11/2000
                PATENT APPLICATION:  US/09/676,135   TIME: 12:29:07

                Input Set : A:\ES.txt
                Output Set: N:\CRF3\10112000\I676135.raw

E--> 597      130                   135                 140
     599 Ser Glu Pro Glu Thr Lys Ala Val Ala Ser Phe Ile Glu Ser Lys Asn
E--> 600 145                 150                 155                 160
     602 Asp Asp Phe Cys Ala
E--> 603                     165
```

VERIFICATION SUMMARY   DATE: 10/11/2000
PATENT APPLICATION: US/09/676,135   TIME: 12:29:08

Input Set : A:\ES.txt
Output Set: N:\CRF3\10112000\I676135.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:573 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
M:332 Repeated in SeqNo=19
L:603 M:252 E: No. of Seq. differs, <211>LENGTH:Input:165 Found:164 SEQ:19
L:748 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22